

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.**

Application Serial Number: 10/564,751  
Source: IFWP  
Date Processed by STIC: 1-30-06

# ***ENTERED***



IFWP

## RAW SEQUENCE LISTING

DATE: 01/30/2006

PATENT APPLICATION: US/10/564,751

TIME: 14:53:45

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Output Set: N:\CRF4\01302006\J564751.raw

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3 <110> APPLICANT: DeveloGen AG fur entwicklungsbiologische Forschung
5 <120> TITLE OF INVENTION: Use of a DG065 secreted protein product for preventing
6     and treating pancreatic diseases and/or obesity and/or
7     metabolic syndrome
9 <130> FILE REFERENCE: 31362PWO_GE
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/564,751
C--> 12 <141> CURRENT FILING DATE: 2006-01-17
14 <150> PRIOR APPLICATION NUMBER: 03016171.5
15 <151> PRIOR FILING DATE: 2003-07-16
17 <150> PRIOR APPLICATION NUMBER: 03016246.5
18 <151> PRIOR FILING DATE: 2003-07-17
20 <150> PRIOR APPLICATION NUMBER: 03016711.8
21 <151> PRIOR FILING DATE: 2003-07-22
23 <150> PRIOR APPLICATION NUMBER: 03018326.3
24 <151> PRIOR FILING DATE: 2003-08-12
26 <160> NUMBER OF SEQ ID NOS: 20
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32 <212> TYPE: DNA
33 <213> ORGANISM: Artificial Sequence
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38 <220> FEATURE:
39 <221> NAME/KEY: gene
40 <222> LOCATION: (1)..(2808)
41 <223> OTHER INFORMATION: nucleic acid sequence encoding human DG008 protein
43 <400> SEQUENCE: 1
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46 ttgacagagc agcagaatat caactccagt agacttgaat gtgcctctgg gcaaagaagc 180
47 agagctaacg aggaaaggga tttaaagagt ttttcttggg tgtttgtcaa acttttattc 240
48 cctgtctgtg tgcagagggg attcaacttc aattttctgc agtggctctg ggtccagccc 300
49 ctactctaaa gatctggaaa gcatgaagac tgggcctttt ttcttatgtc tcttggaac 360
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69 tgaaaatata ggtaccactg agcctggaga gcaccaagag gccaagaaaag cagagaactc 1560
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93 &lt;210&gt; SEQ ID NO: 2

94 &lt;211&gt; LENGTH: 664

95 &lt;212&gt; TYPE: PRT

96 &lt;213&gt; ORGANISM: human

98 &lt;220&gt; FEATURE:

99 &lt;223&gt; OTHER INFORMATION: amino acid sequence of human DG008 protein

101 &lt;400&gt; SEQUENCE: 2

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102 Met Lys Thr Gly Pro Phe Phe Leu Cys Leu Leu Gly Thr Ala Ala Ala
103   1           5           10           15
105 Ile Pro Thr Asn Ala Arg Leu Leu Ser Asp His Ser Lys Pro Thr Ala
106           20           25           30
108 Glu Thr Val Ala Pro Asp Asn Thr Ala Ile Pro Ser Leu Trp Ala Glu
109           35           40           45
111 Ala Glu Glu Asn Glu Lys Glu Thr Ala Val Ser Thr Glu Asp Asp Ser
112           50           55           60
114 His His Lys Ala Glu Lys Ser Ser Val Leu Lys Ser Lys Glu Glu Ser
115   65           70           75           80

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118      85      90      95
120 Leu Lys Asp Gln Glu Asp Ser Asp Gly His Leu Ser Val Asn Leu Glu
121      100      105      110
123 Tyr Ala Pro Thr Glu Gly Thr Leu Asp Ile Lys Glu Asp Met Ile Glu
124      115      120      125
126 Pro Gln Glu Lys Lys Leu Ser Glu Asn Thr Asp Phe Leu Ala Pro Gly
127      130      135      140
129 Val Ser Ser Phe Thr Asp Ser Asn Gln Gln Glu Ser Ile Thr Lys Arg
130 145      150      155      160
132 Glu Glu Asn Gln Glu Gln Pro Arg Asn Tyr Ser His His Gln Leu Asn
133      165      170      175
135 Arg Ser Ser Lys His Ser Gln Gly Leu Arg Asp Gln Gly Asn Gln Glu
136      180      185      190
138 Gln Asp Pro Asn Ile Ser Asn Gly Glu Glu Glu Glu Glu Lys Glu Pro
139      195      200      205
141 Gly Glu Val Gly Thr His Asn Asp Asn Gln Glu Arg Lys Thr Glu Leu
142      210      215      220
144 Pro Arg Glu His Ala Asn Ser Lys Gln Glu Glu Asp Asn Thr Gln Ser
145 225      230      235      240
147 Asp Asp Ile Leu Glu Ser Asp Gln Pro Thr Gln Val Ser Lys Met
148      245      250      255
150 Gln Glu Asp Glu Phe Asp Gln Gly Asn Gln Glu Gln Glu Asp Asn Ser
151      260      265      270
153 Asn Ala Glu Met Glu Glu Glu Asn Ala Ser Asn Val Asn Lys His Ile
154      275      280      285
156 Gln Glu Thr Glu Trp Gln Ser Gln Glu Gly Lys Thr Gly Leu Glu Ala
157      290      295      300
159 Ile Ser Asn His Lys Glu Thr Glu Glu Lys Thr Val Ser Glu Ala Leu
160 305      310      315      320
162 Leu Met Glu Pro Thr Asp Asp Gly Asn Thr Thr Pro Arg Asn His Gly
163      325      330      335
165 Val Asp Asp Asp Gly Asp Asp Asp Gly Asp Asp Gly Gly Thr Asp Gly
166      340      345      350
168 Pro Arg His Ser Ala Ser Asp Asp Tyr Phe Ile Pro Ser Gln Ala Phe
169      355      360      365
171 Leu Glu Ala Glu Arg Ala Gln Ser Ile Ala Tyr His Leu Lys Ile Glu
172      370      375      380
174 Glu Gln Arg Glu Lys Val His Glu Asn Glu Asn Ile Gly Thr Thr Glu
175 385      390      395      400
177 Pro Gly Glu His Gln Glu Ala Lys Lys Ala Glu Asn Ser Ser Asn Glu
178      405      410      415
180 Glu Glu Thr Ser Ser Glu Gly Asn Met Arg Val His Ala Val Asp Ser
181      420      425      430
183 Cys Met Ser Phe Gln Cys Lys Arg Gly His Ile Cys Lys Ala Asp Gln
184      435      440      445
186 Gln Gly Lys Pro His Cys Val Cys Gln Asp Pro Val Thr Cys Pro Pro
187      450      455      460
189 Thr Lys Pro Leu Asp Gln Val Cys Gly Thr Asp Asn Gln Thr Tyr Ala

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190 465          470          475          480
192 Ser Ser Cys His Leu Phe Ala Thr Lys Cys Arg Leu Glu Gly Thr Lys
193          485          490          495
195 Lys Gly His Gln Leu Gln Leu Asp Tyr Phe Gly Ala Cys Lys Ser Ile
196          500          505          510
198 Pro Thr Cys Thr Asp Phe Glu Val Ile Gln Phe Pro Leu Arg Met Arg
199          515          520          525
201 Asp Trp Leu Lys Asn Ile Leu Met Gln Leu Tyr Glu Ala Asn Ser Glu
202          530          535          540
204 His Ala Gly Tyr Leu Asn Glu Lys Gln Arg Asn Lys Val Lys Lys Ile
205 545          550          555          560
207 Tyr Leu Asp Glu Lys Arg Leu Leu Ala Gly Asp His Pro Ile Asp Leu
208          565          570          575
210 Leu Leu Arg Asp Phe Lys Lys Asn Tyr His Met Tyr Val Tyr Pro Val
211          580          585          590
213 His Trp Gln Phe Ser Glu Leu Asp Gln His Pro Met Asp Arg Val Leu
214          595          600          605
216 Thr His Ser Glu Leu Ala Pro Leu Arg Ala Ser Leu Val Pro Met Glu
217          610          615          620
219 His Cys Ile Thr Arg Phe Phe Glu Glu Cys Asp Pro Asn Lys Asp Lys
220 625          630          635          640
222 His Ile Thr Leu Lys Glu Trp Gly His Cys Phe Gly Ile Lys Glu Glu
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231 <211> LENGTH: 2947
232 <212> TYPE: DNA
233 <213> ORGANISM: human
235 <220> FEATURE:
236 <221> NAME/KEY: gene
237 <222> LOCATION: (1)..(2947)
238 <223> OTHER INFORMATION: nucleic acid sequence encoding human DG065 protein
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243 aagataaaga caaggattgt agcttggact gtgcgggttc gcccagaaa cctctctgcg 180
244 catctgacgg aaggaccttc ctttcccgtt gtgaatttca acgtgccaag tgcaaagatc 240
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246 ggaagtatac ccaggagcaa gcccggaagg agtttcagca agtgttcatt cctgagtgca 360
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253 ccctggagga agccaagcag cccaagaacg acaatgtggt gatccctgag tgtgcgcacg 780
254 gcggcctcta caagccagtg cagtgccacc cctccacggg gtactgctgg tgcgtcctgg 840
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293 &lt;210&gt; SEQ ID NO: 4

294 &lt;211&gt; LENGTH: 457

295 &lt;212&gt; TYPE: PRT

296 &lt;213&gt; ORGANISM: human

298 &lt;220&gt; FEATURE:

299 &lt;223&gt; OTHER INFORMATION: amino acid sequence of human DG065 protein

301 &lt;400&gt; SEQUENCE: 4

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306 20 25 30

308 Asp Gln Asp Lys Asp Lys Asp Cys Ser Leu Asp Cys Ala Gly Ser Pro

309 35 40 45

311 Gln Lys Pro Leu Cys Ala Ser Asp Gly Arg Thr Phe Leu Ser Arg Cys

**VERIFICATION SUMMARY**

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date